

## RAW SEQUENCE LISTING

DATE: 01/11/2002

PATENT APPLICATION: US/10/020,095

TIME: 12:55:59

Input Set : A:\LEX-0282-USA SEQLIST.txt

Output Set: N:\CRF3\01112002\J020095.raw

**ENTERED**

3 <110> APPLICANT: Walke, D. Wade  
 4 Scoville, John  
 5 Turner, C. Alexander Jr.  
 7 <120> TITLE OF INVENTION: Novel Human Alpha Macroglobulin Family Proteins and Polynucleotides  
 8 Encoding the Same  
 10 <130> FILE REFERENCE: LEX-0282-USA  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/020,095  
 C--> 12 <141> CURRENT FILING DATE: 2001-12-14  
 12 <150> PRIOR APPLICATION NUMBER: US 60/255,566  
 13 <151> PRIOR FILING DATE: 2000-12-14  
 15 <160> NUMBER OF SEQ ID NOS: 5  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 4338  
 21 <212> TYPE: DNA  
 22 <213> ORGANISM: homo sapiens  
 24 <400> SEQUENCE: 1

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26	gccgtggctc	ccgggcctcg	gtttctgggt	acagccccag	ggatcatcag	gcccggagga	120
27	aatgtgacta	ttgggggtgga	gcttctggaa	cactgccctt	cacaggtgac	tgtgaaggcg	180
28	gagctgctca	agacagcctc	aaacctcact	gtctctgtcc	tggaagcaga	aggagtcttt	240
29	gaaaaaggct	cttttaagac	acttactctt	ccatcactac	ctctgaacag	tgcagatgag	300
30	atttatgagc	tacgtgtaac	cggacgtacc	caggatgaga	ttttattctc	taatagtacc	360
31	cgcttatcat	ttgagaccaa	gagaatatct	gtcttcattc	aaacagacaa	ggccttatac	420
32	aagccaaagc	aagaagtga	gtttcgcatt	gttacactct	tctcagattt	taagccttac	480
33	aaaacctctt	taaacattct	cattaaggac	cccaaataca	atttgatcca	acagtgggtg	540
34	tcacaacaaa	gtgatcttgg	agtcatttcc	aaaacttttc	agctatcttc	ccatccaata	600
35	cttggtgact	ggctatttca	agttcaagt	aatgaccaga	catattatca	atcatttcag	660
36	gtttcagaat	atgtattacc	aaaatttgaa	gtgactttgc	agacaccatt	atattgttct	720
37	atgaattcta	agcattttaa	tggtaccatc	acggcaaagt	atacatatgg	gaagccagtg	780
38	aaaggagacg	taacgcttac	atttttacct	ttatcctttt	ggggaaagaa	gaaaaatatt	840
39	acaaaaacat	ttaagataaa	tggaactgca	aacttctctt	ttaatgatga	agagatgaaa	900
40	aatgtaatgg	attcttcaaa	tggaacttct	gaataacctg	atctatcttc	ccctggacca	960
41	gtagaaattt	taaccacagt	gacagaatca	gttacaggta	tttcaagaaa	tgtaagcact	1020
42	aatgtgttct	tcaagcaaca	tgattacatc	attgagtttt	ttgattatac	tactgtcttg	1080
43	aagccatctc	tcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg	1140
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45	tactggagcg	gatctaacag	tggaatcag	aaaatggaag	ctgttcagaa	aataaattat	1260
46	actgtccccc	aaagtggaa	ttttaagatt	gaattcccaa	tcctggagga	ttccagttag	1320
47	ctacagttga	aggcctatct	ccttggtagt	aaaagtagca	tggcagttca	tagtctgttt	1380
48	aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga	1440
49	tcgccttttg	agttgggtgt	tagtggcaac	aaacgattga	aggagttaag	ctatatggta	1500
50	gtatccaggg	gacagttggt	ggctgtagga	aaacaaaatt	caacaatggt	ctctttaaca	1560
51	ccagaaaatt	cttggaactcc	aaaagcctgt	gtaattgtgt	attatattga	agatgatggg	1620
52	gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag	1680
53	ctatattgga	gtaaagtga	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg	1740
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55 gcctctaattg atattacaat ggaaaatgtg gtccatgagt tggaaacttta taacacagga 1860
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57 ttgacagatg caaacctcac gaaggattat attgatgggtg tttatgacaa tgcagaatat 1980
58 gctgagaggt ttatggagga aaatgaagga catattgtag atattcatga cttttctttg 2040
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60 atgggttaca ggattttacca agaatttgaa gtaactgtac ctgattctat cacttcttgg 2160
61 gtggctactg gttttgtgat ctctgaggac ctgggtcttg gactaacaac tactccagt 2220
62 gagctccaag ccttccaacc atttttcatt tttttgaatc ttccctactc tgttatcaga 2280
63 ggtgaagaat ttgctttgga aataactata ttcaattatt tgaaagatgc cactgagggt 2340
64 aaggtaatca ttgagaaaag tgacaaaatt gatattctaa tgacttcaag tgaaataaat 2400
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67 gcttctgatg ctgtcaccca gatgatttta gtaaaggctg aaggaataga aaaatcatat 2580
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69 agtttctcat ttctctctaa tacagtgact ggcagtgaag gagttcagat cactgcaatt 2700
70 ggagatgttc ttggtccttc catcaatggc ttgacctcat tgattcggat gccttatggc 2760
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76 cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gcttcaagg 3120
77 ggcaataaaa gtccagtaac acttacagcc tataattgaa cttctctctc gggatataga 3180
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79 agaggaattt cagacaatta tactctagcc cttataactt atgcattgtc atcagtggg 3300
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99 <210> SEQ ID NO: 2
100 <211> LENGTH: 1445
101 <212> TYPE: PRT
102 <213> ORGANISM: homo sapiens
104 <400> SEQUENCE: 2
105 Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys

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106 1          5          10          15
107 Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
108          20          25          30
109 Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
110          35          40          45
111 Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
112          50          55          60
113 Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
114 65          70          75          80
115 Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
116          85          90          95
117 Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
118          100          105          110
119 Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
120          115          120          125
121 Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
122          130          135          140
123 Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
124 145          150          155          160
125 Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
126          165          170          175
127 Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr
128          180          185          190
129 Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val
130          195          200          205
131 Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr
132          210          215          220
133 Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser
134 225          230          235          240
135 Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr
136          245          250          255
137 Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser
138          260          265          270
139 Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly
140          275          280          285
141 Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp
142          290          295          300
143 Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Ser Pro Gly Pro
144 305          310          315          320
145 Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg
146          325          330          335
147 Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu
148          340          345          350
149 Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala
150          355          360          365
151 Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu
152          370          375          380
153 Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu
154 385          390          395          400

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155 Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln
156          405          410          415
157 Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe
158          420          425          430
159 Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu
160          435          440          445
161 Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser
162          450          455          460
163 Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
164 465          470          475          480
165 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
166          485          490          495
167 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
168          500          505          510
169 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
170          515          520          525
171 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
172          530          535          540
173 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
174 545          550          555          560
175 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
176          565          570          575
177 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
178          580          585          590
179 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
180          595          600          605
181 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
182          610          615          620
183 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
184 625          630          635          640
185 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
186          645          650          655
187 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
188          660          665          670
189 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
190          675          680          685
191 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Tyr Arg
192          690          695          700
193 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
194 705          710          715          720
195 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
196          725          730          735
197 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu
198          740          745          750
199 Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile
200          755          760          765
201 Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile
202          770          775          780
203 Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn

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205 Ala Thr Gly His Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala
206          805          810          815
207 Thr Val Leu Phe Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile
208          820          825          830
209 Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Val Thr Gln Met
210          835          840          845
211 Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile
212          850          855          860
213 Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu
214 865          870          875          880
215 Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln
216          885          890          895
217 Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala
218          900          905          910
219 Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn
220          915          920          925
221 Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln
222          930          935          940
223 Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly
224 945          950          955          960
225 Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala
226          965          970          975
227 Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val
228          980          985          990
229 Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn
230          995          1000          1005
231 Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn
232          1010          1015          1020
233 Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
234 1025          1030          1035          1040
235 Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
236          1045          1050          1055
237 Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
238          1060          1065          1070
239 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
240          1075          1080          1085
241 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
242          1090          1095          1100
243 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
244 1105          1110          1115          1120
245 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
246          1125          1130          1135
247 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
248          1140          1145          1150
249 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
250          1155          1160          1165
251 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
252          1170          1175          1180

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VERIFICATION SUMMARY

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Input Set : A:\LEX-0282-USA SEQLIST.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date